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RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/833,041   TIME: 11:17:07

     Input Set : A:\PF545SL.txt
     Output Set: N:\CRF3\04302001\I833041.raw

```
   5 <110> APPLICANT: Rosen, Craig A.
   6         Haseltine, William A.
   8 <120> TITLE OF INVENTION: Albumin Fusion Proteins
  10 <130> FILE REFERENCE: PF545
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/833,041
  13 <141> CURRENT FILING DATE: 2001-04-12
  15 <150> PRIOR APPLICATION NUMBER: 60/229,358
  16 <151> PRIOR FILING DATE: 2000-04-12
  18 <150> PRIOR APPLICATION NUMBER: 60/256,931
  19 <151> PRIOR FILING DATE: 2000-12-21
  21 <150> PRIOR APPLICATION NUMBER: 60/199,384
  22 <151> PRIOR FILING DATE: 2000-04-25
  24 <160> NUMBER OF SEQ ID NOS: 79
  26 <170> SOFTWARE: PatentIn Ver. 2.1
  28 <210> SEQ ID NO: 1
  29 <211> LENGTH: 23
  30 <212> TYPE: DNA
  31 <213> ORGANISM: Artificial Sequence
  33 <220> FEATURE:
  34 <221> NAME/KEY: primer_bind
  35 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
  37 <400> SEQUENCE: 1
  38 cccaagaatt cccttatcca ggc                                    23
  41 <210> SEQ ID NO: 2
  42 <211> LENGTH: 33
  43 <212> TYPE: DNA
  44 <213> ORGANISM: Artificial Sequence
  46 <220> FEATURE:
  47 <221> NAME/KEY: primer_bind
  48 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
  50 <400> SEQUENCE: 2
  51 gggaagctta gaagccacag gatccctcca cag                         33
  54 <210> SEQ ID NO: 3
  55 <211> LENGTH: 16
  56 <212> TYPE: DNA
  57 <213> ORGANISM: Artificial Sequence
  59 <220> FEATURE:
  60 <221> NAME/KEY: misc_structure
  61 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
  62         with non-cohesive ends.
  64 <400> SEQUENCE: 3
  65 gataaagatt cccaac                                            16
  68 <210> SEQ ID NO: 4
  69 <211> LENGTH: 17
  70 <212> TYPE: DNA
  71 <213> ORGANISM: Artificial Sequence
  73 <220> FEATURE:
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 74 <221> NAME/KEY: misc_structure
 75 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 76       with non-cohesive ends.
 78 <400> SEQUENCE: 4
 79 aattgttggg aatcttt                                              17
 82 <210> SEQ ID NO: 5
 83 <211> LENGTH: 17
 84 <212> TYPE: DNA
 85 <213> ORGANISM: Artificial Sequence
 87 <220> FEATURE:
 88 <221> NAME/KEY: misc_structure
 89 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 90       with non-cohesive ends.
 92 <400> SEQUENCE: 5
 93 ttaggcttat tcccaac                                              17
 96 <210> SEQ ID NO: 6
 97 <211> LENGTH: 18
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <221> NAME/KEY: misc_structure
103 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
104       with non-cohesive ends.
106 <400> SEQUENCE: 6
107 aattgttggg aataagcc                                             18
110 <210> SEQ ID NO: 7
111 <211> LENGTH: 24
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <221> NAME/KEY: SITE
117 <222> LOCATION: 1)..(19)
118 <223> OTHER INFORMATION: invertase leader sequence
120 <220> FEATURE:
121 <221> NAME/KEY: SITE
122 <222> LOCATION: 20)..(24)
123 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
125 <400> SEQUENCE: 7
126 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
127   1               5                  10                  15
129 Ile Ser Ala Asp Ala His Lys Ser
130               20
133 <210> SEQ ID NO: 8
134 <211> LENGTH: 21
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <221> NAME/KEY: misc_structure
140 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
```

```
141        fragments with non-cohesive ends.
143 <400> SEQUENCE: 8
144 gagatgcaca cctgagtgag g                                        21
147 <210> SEQ ID NO: 9
148 <211> LENGTH: 27
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <221> NAME/KEY: misc_structure
154 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
155        fragments with non-cohesive ends.
157 <400> SEQUENCE: 9
158 gatcctgtgg cttcgatgca cacaaga                                  27
161 <210> SEQ ID NO: 10
162 <211> LENGTH: 24
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <221> NAME/KEY: misc_structure
168 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
169        fragments with non-cohesive ends.
171 <400> SEQUENCE: 10
172 ctcttgtgtg catcgaagcc acag                                     24
175 <210> SEQ ID NO: 11
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <221> NAME/KEY: misc_structure
182 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
183        fragments with non-cohesive ends.
185 <400> SEQUENCE: 11
186 tgtggaagag cctcagaatt tattcccaac                                30
189 <210> SEQ ID NO: 12
190 <211> LENGTH: 31
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <221> NAME/KEY: misc_structure
196 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
197        fragments with non-cohesive ends.
199 <400> SEQUENCE: 12
200 aattgttggg aataaattct gaggctcttc c                              31
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 47
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <221> NAME/KEY: misc_structure
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```
210 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
211       fragments with non-cohesive ends.
213 <400> SEQUENCE: 13
214 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac            47
217 <210> SEQ ID NO: 14
218 <211> LENGTH: 48
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <221> NAME/KEY: misc_structure
224 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
225       fragments with non-cohesive ends.
227 <400> SEQUENCE: 14
228 aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc           48
231 <210> SEQ ID NO: 15
232 <211> LENGTH: 62
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <221> NAME/KEY: misc_structure
238 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
239       fragments with non-cohesive ends.
241 <400> SEQUENCE: 15
242 ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcggtgg atccttccca 60
243 ac                                                             62
246 <210> SEQ ID NO: 16
247 <211> LENGTH: 63
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_structure
253 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
254       fragments with non-cohesive ends.
256 <400> SEQUENCE: 16
257 aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
258 gcc                                                            63
261 <210> SEQ ID NO: 17
262 <211> LENGTH: 1782
263 <212> TYPE: DNA
264 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(1755)
271 <400> SEQUENCE: 17
272 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa   48
273 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
274  1               5                   10                  15
276 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag   96
277 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
```

```
278              20              25              30
280 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa    144
281 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
282         35              40              45
284 ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa    192
285 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
286         50              55              60
288 tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt    240
289 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
290    65              70              75              80
292 cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct    288
293 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
294         85              90              95
296 gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc    336
297 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
298         100             105             110
300 ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat    384
301 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
302         115             120             125
304 gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga    432
305 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
306         130             135             140
308 aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg    480
309 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
310 145             150             155             160
312 tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc    528
313 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
314             165             170             175
316 tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg    576
317 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
318         180             185             190
320 tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa    624
321 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
322         195             200             205
324 aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc    672
325 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
326         210             215             220
328 aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa    720
329 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
330 225             230             235             240
332 gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac    768
333 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
334             245             250             255
336 agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc    816
337 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
338         260             265             270
340 agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac    864
341 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
342         275             280             285
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/833,041

DATE: 04/30/2001
TIME: 11:17:08

Input Set : **A:\PF545SL.txt**
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```
L:12   M:270 C: Current Application Number differs, Replaced Current Application Number
L:711  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:800  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:889  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:979  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
```